

Similarities in sequence between the dnaA homolog and sequences deposited in public sequence databases.

Sequences producing significant alignments:		Score (bits)	E Value
gi 140025 sp P06567 DNAI_BACSU PRIMOSOMAL PROTEIN DNAI	>gi 2797...	231	5e-60
gi 468268 (M15183) ORFY [Bacillus subtilis]		125	5e-28
gi 2072367 emb CAA70453 (Y09255) primosomal protein DnaI [Baci...		84	1e-15
gi 530419 emb CAA83732 (Z33058) GTP bind. CD48/PAS1/SEC18 fam...		67	2e-10
gi 2983431 (AE000713) DNA replication protein DnaC [Aquilifex aeo...		52	4e-06
gi 1176732 sp P45910 YOAM_BACSU HYPOTHETICAL 36.1 KD PROTEIN IN...		50	2e-05
gi 2127076 pir 140411 hypothetical protein 5 (xre region) - Ba...		48	1e-04
gi 1722861 sp P39782 XKDC_BACSU PHAGE-LIKE ELEMENT PBSX PROTEIN...		48	1e-04
gi 1353529 (U38906) ORF12 [Bacteriophage rlt]		46	4e-04
gi 2983000 (AE000683) chromosome replication initiator protein ...		45	8e-04
<p>>gi 140025 sp P06567 DNAI_BACSU PRIMOSOMAL PROTEIN DNAI</p> <p>>gi 279708 pir IQBS44 dnaA protein homolog, 44K -</p> <p>Bacillus subtilis >gi 39881 emb CAA28633 (X04963) ORF</p> <p>311 (AA 1-311) [Bacillus subtilis]</p> <p>>gi 1769996 emb CAA99605 (Z75208) replication protein</p> <p>[Bacillus subtilis] >gi 2293281 (AF008220) DnaI</p> <p>[Bacillus subtilis] >gi 2635363 emb CAB14858 (Z99118)</p> <p>helicase loader [Bacillus subtilis]</p> <p>Length = 311</p>			
<p>Score = 231 bits (583), Expect = 5e-60</p> <p>Identities = 120/280 (42%), Positives = 177/280 (62%), Gaps = 2/280 (0%)</p>			
<p>Query: 35 DPDVKQFLEAHRAELTNAMIDEDLNVLQEQYKDQKHYDG-HKFDPCPNFVKGHVPELYVD 93</p> <p>D DV+ FL+ + + MI++ LN L EY +Q K+ + +C N ++G+ P+L V+</p> <p>Sbjct: 31 DQDVQAFKENEVIDQKMIKSLNKLYEYIEQSKNCSYCSDEDENCNLLGYHPKLVVN 90</p>			
<p>Query: 94 NNRIKIRYLQCPCKIKYDEERFEALITSHHMORDTLNAKLKDIYMNRDRDLVMAAADD 153</p> <p>I I Y +CP K K D+++ + L+ S ++Q-D L A + + -- RL + D</p> <p>Sbjct: 91 GRSIDIEYYECPVRRKLDQKKQCSLMKSMYIQDQLLGATFQQVDISDPSRLAMFQHVTD 150</p>			
<p>Query: 154 ICTAITNGEQVKGLYLYGPFGTGKSFILGAIANQLKSKKVRSTIYLPEFIRTLKGGFKD 213</p> <p>+ + KGLYLYG FG GK+F+L AIAN+L K+ S I+Y+PEF+R LK +D</p> <p>Sbjct: 151 FLKSYNETGKGLYLYGKFGVGKTFMLAAIANELAEKEYSSMIVVPEFVRELKNSLQD 210</p>			
<p>Query: 214 GSFEKKLHRVREANIIMLDDIGAEVTPWVRDEVIGPLLHYRMVHELPTFFSSNFDYSEL 273</p> <p>+ E+KL+ V+ +LMLDDIGAE +T WVRDEVIG +L +RM +LPTFFSSNF EL</p> <p>Sbjct: 211 QTLEEKLNVMVKTTPVLMDDIGAESMTSWVRDEVIGTVLQHRMSQQLPTFFSSNFSDEL 270</p>			
<p>Query: 274 EHHLAMTRDGE-EKTKAARIIRVKSLSPTYFLSGENFRN 312</p> <p>+HH ++ GE E- KAAR++ER+ L+ P L GEN R+</p> <p>Sbjct: 271 KHHFTYSQRGEKEEVKAARLMERILYLAAPIRLDGENRRH 310</p>			
<p>>gi 468268 (M15183) ORFY [Bacillus subtilis]</p> <p>Length = 207</p>			
<p>Score = 125 bits (310), Expect = 5e-28</p> <p>Identities = 67/190 (35%), Positives = 105/190 (55%), Gaps = 1/190 (0%)</p>			
<p>Query: 20 DFXXXXXXXXXXXXNDPVKQFLEAHRAELTNAMIDEDLNVLQEQYKDQKHYDG-HKFD 78</p> <p>DF D DV+ FL+ + + MI++ LN L EY +Q K+ + +</p> <p>Sbjct: 16 DFQNRLEQTKKVKMDQDVQAFKENEVIDQKMIKSLNKLYEYIEQSKNCSYCSDEDEN 75</p>			
<p>Query: 79 CPNFVKGHVPELYVDNNRIKIRYLQCPCKIKYDEERFEALITSHHMORDTLNAKLKDIY 138</p> <p>C N ++G+ P+L V- I I Y +CP K K D+++ + L+ S ++Q-D L A + +</p> <p>Sbjct: 76 CNNLLEGYHPKLVVNGRSIDIEYYECPVRRKLDQKKQCSLMKSMYIQDQLLGATFQQVD 135</p>			
<p>Query: 139 MNHRDRDLVMAAADDICTAITNGEQVKGLYLYGPFGTGKSFILGAIANQLKSKKVRSTII 198</p> <p>++ RL + D + + KGLYLYG FG GK+F+L AIAN+L K+ S I+</p> <p>Sbjct: 136 ISDPSRLAMFQHVTDFLKSYNETGKGLYLYGKFGVGKTFMLAAIANELAEKEYSSMIV 195</p>			
<p>Query: 199 YLPEFIRTLK 208</p> <p>Y+PEF+R LK</p> <p>Sbjct: 196 YVPEFVRELK 205</p>			

002107"25668960

A.

SEQ ID NO:1

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121    tttttggaag cgcacgcagc tgaattaacg aatgctatga ttgatgaaga cttaaatgtg
181    ttacaagagt ataaagatca acaaaaacat tatgacggtc ataaatttgc tgattgtcca
241    aatttcgtaa aggggcatgt gcctgagtta tatgttgata ataaccgaat taaaatacgc
301    tatttacaat gcccacgtaa aatcaagtac gacgaagaac gctttgaagc tgagctaatt
361    acatctcatc atatgcaacg agatacttta aatgccaaat tgaaagatat ttatatgaat
421    catcgagacc gtcttgatgt agctatggca gcagatgata tttgtacagc aataactaat
481    ggggaacaag tgaaaggcct ttacctttat ggtccatttg ggacaggtaa atcttttatt
541    ctaggtgcaa ttgcgaatca gctcaaatct aagaaggtag gttcgacaat tatttattta
601    ccggaattta ttagaacatt aaaagggtggc tttaaagatg gttcttttga aaagaaatta
661    catcgcgtaa gagaagcaaa cattttaatg cttgatgata ttggggctga agaagtgact
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781    ccaacattct ttagttctaa ttttgactat agtgaattgg aacatcattt agcgatgact
841    cgtgatggtg aagagaagac taaagcagca cgtattattg aacgtgtcaa atctttgtca
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SEQ ID NO:2

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121    TSHHMQRDTL NAKLKDIYMN HRDRLDVAMA ADDICTAITN GEQVKGLYLY GPFGTGKSFI
181    LGAIANQLKS KKVRSIIYLL PEFIRTLKGG FKDGSEFEKKL HRVREANILM LDDIGAEVET
241    PWVRDEVIGP LLHYRMVHEL PTFFSSNFDY SELEHHLAMT RDGEEKTKAA RIIERVKSLS
301    TPYFLSGENF RNN

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Fig. 1

0958956.101200

SEQ ID NO : 3

Complete genome sequence of bacteriophage 77

1 gatcaaaata cttggggaac gggttagggag taaacttcgc gataatttta aaaattcatg
 61 tataaccccc ctcttataac cattttaagg caggtgatga aatggagatt atagtcgatg
 121 aaaatttagt gcttaaagaa aaagaaaggc tacaagtatt atataaagac atacctagca
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 241 attacatgtg ggaagacata aaagaaagag gtgattatga tttatttact caatctgaaa
 301 aggcgccacc atatgaaagg gaaagaccag tagccaaact atttaatgct agagatgctg
 361 catatcaaaa aataatcaaa caattatcgg atttattgcc cgaagagaaa gaagacacag
 421 aaacgccatc tgatgattac ctatgattag taataaatac gttgatgaat atataaattt
 481 gtggaaacaa ggaaagataa ttttaataaa agaaagaatt gatctcttta attatctaca
 541 aaaacatata tattcacgag atgatgtata ttttgatgaa cagaaaatcg aggattgtat
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 781 cttacacgga gttaaagaat atcacatctc cattgttgct aatagtgaag atcaagcaaa
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 1141 gggttatata gatgcaatga agcacaatat tgcaagtgtt ttaagtggca aggttaaaaa
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 1561 cgatgattac atttggttag gacattcgtt tgtaagacaa gggtttttgg atgatgtcaa
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 3001 gaacgaatta aacgcgaaac tcataacaca aagcatgtat ttgaaagata caagaataga
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 5641 aagaattgat acttatacgc gctagatatg cttatcaaga tttattagaa cacttcaacg
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7081	aaaaacagct	tatgctgatg	gcggtccaat	tgaatcaggg	aatacagacg	gagaaggtaa
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7261	atgggttcaga	caagagcgta	aagacggtac	atttagaaca	gttttattac	ctaaagttaa
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8581	attctgactt	aaaattaaca	ggcaacaact	tcaaataatac	cgaaaaatca	actgatagtt
8641	acaaacaaag	gattaaagaa	cttgatggaa	ctatcacagg	ttataagaaa	aacgttgatg
8701	atthagccaa	gcaatatgac	aaggatatct	aagaacaggg	cgaaaacagt	gcagaagctc
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8821	tacaaaaaac	atcagccgaa	tttgaagagt	tcaaaaaaagc	tcaagttgaa	gctcaaagaa
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37621 agaaagcgca agcgtttgat gaaatacttg agggaatgac aaatgctatt caacattcag
37681 ttaaagaagg tattgaactt gatgaagcag tagggattat ggcaggtcag gttgtctata
37741 aatatgagga ggaataggaa aatgactaac acattacaag taaaactatt atcaaaaaat
37801 gctagaatgc ccgaacgaaa tcataagacg gatgcagggt atgacatatt ctcagctgaa
37861 actgtcgtac tcgaaccaca agaadaagca gtgatcaaaa cagatgtagc tgtgagtata
37921 ccagagggct atgtcggact attaactagt cgtagtgggt taagtagtaa aacgtattta
37981 gtgattgaaa caggcaagat agacgcggga tatcatggca atttagggat taatatcaag
38041 aatgatgaag aacgtgatgg aatacccttt ttatatgatg atatagacgc tgaattagaa
38101 gatggattaa taagcatttt agatataaaa ggtaactatg tacaagatgg aagaggcata
38161 agaagagttt accaaatcaa caaaggcgat aaactagctc aattggttat cgtgcctata
38221 tggacaccgg aactaaagca agtggaggaa ttcgaaagtg tttcagaacg tggagcaaaa
38281 ggcttcggaa gtagcggagt gtaaagacat cttagatcga gttaaggagg ttttggggaa
38341 gtgacgcaat acttagtcac aacattcaaa gattcaacag gacgaccaca tgaacatatt
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38521 gaaaatataa gggagtgtgg gaaatgacgg atgttaaaat taaaactatt tcaggtggag
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38641 atggttatat ttacgcaagt actataatca agaaaccaac gtatattaaa acagatacga
38701 ttgaatcaat cacacttatt gaggagcatg ggaaatgaat cagctgagaa ttttattaca
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39001 cacctgaaga aaaggctaag attgaagatg attttattaa agaaattaaa gataaagaca
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39121 gaatgatgcc tagtttaatt gatactggag atgacaatga tgattaaaaa acttaaaaat
39181 atggatgggt tcgacatctt tattgttggg atactgtcat tattcgggat attcgcattg
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39301 caaggaacta ttacagataa atataacaag agacaagata aagaagacaa gttctatatt
39361 gtattagaca acaacaagt cattgaaaat tccgacttat tattcaaaa gaaatttgat
39421 agcgcagata tacaagctag gttaaaagta ggcgataagg tagaagttaa aacaatcggg
39481 tatagaatac acttttttaa tttatatccg gtctttatag aagtaaagaa ggtagataaa
39541 caatgattaa acaataacta agactattat tcttactagc aatgtatgag ttaggtaagt
39601 attgaactga gcaagtgtat attatgatga cggctaata tgaatgaata tttatttatg
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39901 gctttattca gttaaagaga tttttaggta ttttacagat tctaacttac aacgtaaaaa
39961 aatcaattta gaacaaatat atccgatata tttagattgt tttaaaaagg ctaaaaagat
40021 gattggagct tatattatcc caacagaaca gcatgaattt ttagattttt ttgatattga
40081 agtctttaat aatttagata agcaaagtaa aaaagcgtat gaaaatgtta ttggatttag
40141 acaaatgatt aatttatcaa atagagttaa ggcaatggaa gattttaaga tgagtttcaa
40201 caatgaattt agtacaaatc agattttttt taatccttct tttgttatgg aaacaattgc
40261 tattataaat gaatatcaaa aagatatatc ttatttaaaa aatataatta ataaaaatgaa
40321 tgaaaataga gcttataatc atattgatag ttttatcact tcagagtacc gacgaaaaat
40381 aaacgattat aatctttatc ttgataaatt tgaagaacag tttagtcaaa agtttaaaat
40441 aaacagaact tcgataaaaag aaagaattat tattaattta aacaagagga gatttaaatg
40501 atgtggatta ctatgactat tgtatttgct atattgctat tagtttgat cagttaaatg
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40621 gtagttaaaa ctaaaagggt caacgggtta gaagaataca ggattgaatt gaagcgaatg
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40741 gagaaacacg atatcaaaaa gcttgaagaa tacattcagc acatcgataa ctatcgaaga
40801 gagttgaaga tgcgagaata tgaattactt gaaagtcatg aaccagataa tgcgggagct

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40861	ggcaaaaagta	atttgccggg	taaccgcgatt	gaacgatgtg	caataaagaa	gtttagtgat
40921	aacagggtaca	atacattaag	aaatatagtt	aacgggtgtag	atagattgat	agggtgaaagt
40981	gatgaggata	cgcttgagtt	attaaggttt	agatattggg	attgtcctat	tggttgttat
41041	gaatgggaag	atatagcaca	ttactttggt	acaagtaaga	caagtatatt	acgtagaagg
41101	aatgcactga	tcgataagtt	agcaaagtat	attgggttatg	tgtagcggac	ttttacccta
41161	tgtaaagtccg	cattaaaaca	gtttattatg	ttagtatcag	attaatatatt	aaagttatta
41221	aatgctaata	cgacgcgatga	acaagaggcg	catcactatg	tgatgtgtct	ttttatttat
41281	gaggatgaa	catgttcaaa	ctaattgtaa	atacattact	acacatcaag	tatagatgag
41341	tcttgatact	acttaagtta	tataagggtga	aacattatga	tgactaaaga	cgaacgtata
41401	cgattctata	agtctaaaga	atggcaaata	acaagaaaaa	gagtgtctaga	aagagataat
41461	tatgaatgtc	aacaatgtaa	gagagacggc	aagttaacga	catatgacaa	aagcaagcgt
41521	aatgcgttgg	atgtagatca	tatattataa	ctagaacatc	atccggagtt	tgctcatgac
41581	ttaaacaatt	tagaaacact	gtgtatttaa	tgtcacaaaca	aaaaagaaaa	gagatttata
41641	aaaaaagaaa	ataaatggaa	agacgaaaaa	tggtaaatac	ccccgggtca	aaaaaatcaa
41701	aagcgatc					

ORF: 2368950

Phage: Bacteriophage 77
 Minimal ORF size: 33 a.a.
 ORFs "with" RBS:
 Number of ORFs: 99

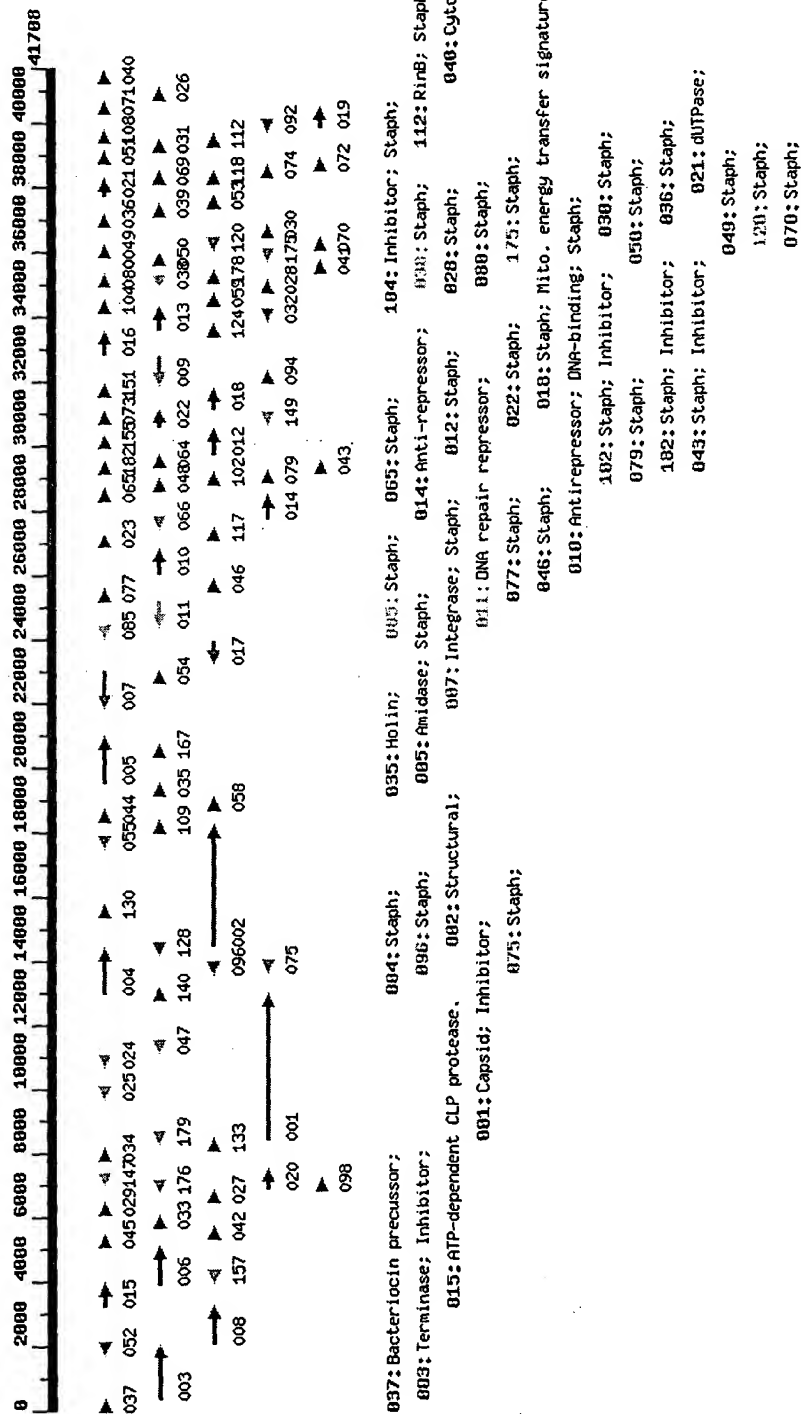


Fig. 4

P77ORF104

SEQ ID NO: 4

```
1   atggtaacca aagaattttt aaaactaaa cttgagtgtt cagatatgta cgctcagaaa
61  ctcatagatg aggcacaggg cgatgaaaat aggttgtagc acctatttat ccaaaaactt
121 gcagaacgtc atacacgccc cgctatcgtc gaatattaa
```

SEQ ID NO: 5

```
1   MVTKEFLKTK LECSDMYAQK LIDEAQGDEN RLYDLFIQKL AERHTRPAIV EY
```

002101 2566960

Fig. 5

Predicted Tryptic Peptide Masses of Conceptual ORF in Contig 1383:

1 MGGGQSIMKqfkSIINTSQDFEKrlEKikkK 30
 31 evindpdvkQFLEAHRAeiltnamidedinv 60
 61 lqeykDQQKhdyghkFADCPNFVKghvpel 90
 91 yvdnnrIKirYLQCPCKikyDEERfeaeli 120
 121 tsnnmqrDTLNAKikDIYMNHRdrLDVAMA 150
 151 ADDICTAITNGEQVKglylygpgfgtgkSFI 180
 181 LGAIANQLKskKvrSTIIYLPEFIRtikGG 210
 211 FKdgsfekKihrvReannilmiddigaeet 240
 241 pwvrDEVIGPLLHYRmvhelptffssnfdy 270
 271 selehhlamtrDGEEKtkAARierVKsls 300
 301 tpyflsgenfrNN 313

Tryptic peptide fragment:

GHVPELYVDNNR

Predicted Peptide Mass MH+ = 1413.538

STIIYLPEFIR

Predicted Peptide Mass MH+ = 1352.6221

SLSTPYFLSGENFR

Predicted Peptide Mass MH+ = 1618.7923

002707 25658950

A.

SEQ ID NO: 6 DnaC nucleotide *B. subtilis*

1 atgacagacc ttctgaatga cgggcttcct cgcacaaata tagaagccga
 51 acaagccgtg ttaggcgcta tttttttaca gccgtctgct ttaacactgg
 101 cttcagaagt attgattcca gatgatttct atagaatgtc ccaccaaaaa
 151 atctataatg cgatgctggt gctcggtgac cgaggtgaac cggttgatct
 201 ggtgacagtt acatcagagc ttgcgaacac agacctgctg gaagaagtag
 251 gcggtatttc atatttgaca gatatcgcaa actcggtgcc gacagcggct
 301 aacatagaat attacgcgaa aatcgttgag gaaaaatcga ttcttcgccg
 351 attaatacaga actgcgacaa cgattgctca agacgggtat acccgtgagg
 401 atgaggtcga ggatttactc agtgaagcgg aaaaaacgat tatggaagtg
 451 gcacagcgca aaaacacgag tgccttccaa aatattaagg acgtccttgt
 501 ccagacctat gataatatcg aacagcttta caatcgaaaa ggtgatataca
 551 cgggaattcc aacagggttt acggagcttg accggatgac tgcgggtttc
 601 cagcgcaacg acttgatcat tgtggctgcc cgtccttcag tagggaaaac
 651 agcctttgcc ctgaacatcg cacaaaacgt ggcgacgaag accgatgaga
 701 gcgtagcgaat tttcagtcct gagatgggtg ccgagcagct cgttatgcgt
 751 atgctctgtg ccgagggaaa tatcaatgcc cagaatctcc gtacaggtaa
 801 cctgaccgaa gaggattggg gcaagctgac gatggcaatg ggaagcctat
 851 cgaacagcgg gatttacatc gatgatacac cgggtattcg agtgagtga
 901 atccgtgcc aagtgcgcgc cttgaagcag gaaagcgggc tgggcatgat
 951 tttgatcgat tacctgcaat tgattcaggg aagcggtcgt tcaaaggaca
 1001 accgtcagca ggaagtatct gaaatttccc gtgaactgaa gtcgattgag
 1051 agggagctgc aagtccctgt tatcgcgctt tctcagcttt ccagggggtg
 1101 tgagcagcgt caggataaac gtccgatgat gtctgatata cgggaatcag
 1151 gaagtatcga gcaggacgcg gatattgtcg cgttccttta tcgtgatgac
 1201 tactatgaca aagaaaccga gaataaaaat attatcgaat ttattatcgc
 1251 caaacagcgt aacggcccg taggaaccgt gtctcttgcg ttcgtaaaag
 1301 aatacaacaa attcgtcaac ctggaacggc gttttgatga cgcaggcggt
 1351 ccgccccggc ca

SEQ ID NO: 7 DnaC nucleotide *S. aureus*

1 ATGGATAGAA TGTATGAGCA AAATCAAATG CCGCATAACA ATGAAGCTGA
 51 ACAGTCTGTC TTAGGTTCAA TTATTATAGA TCCAGAATTG ATTAATACTA
 101 CTCAGGAAGT TTTGCTTCCT GAGTCGTTTT ATAGGGGTGC CCATCAACAT
 151 ATTTTCCGTG CAATGATGCA CTAAATGAA GATAATAAAG AAATTGATGT
 201 TGTAACATTG ATGGATCAAT TATCGACGGA AGGTACGTTG AATGAAGCGG
 251 GTGGCCCGCA ATATCTTGCA GAGTTATCTA CAAATGTACC AACGACGCGA
 301 AATGTTCAAT ATTATACTGA TATCGTTTCT AAGCATGCAT TAAAACGTAG
 351 ATTGATTCAA ACTGCAGATA GTATTGCCAA TGATGGATAT AATGATGAAC
 401 TTGAAGTAGA TGCGATTTTA AGTGATGCAG AACGTCGAAT TTTAGAGCTA
 451 TCATCTTCTC GTGAAAGCGA TGGCTTTAAA GACATTCGAG ACGTCTTAGG
 501 ACAAGTGTAT GAAACAGCTG AAGAGCTTGA TCAAAATAGT GGTCAAACAC
 551 CAGGTATACC TACAGGATAT CGAGATTAG ACCAAATGAC AGCAGGGTTC
 601 AACCGAAATG ATTTAATTAT CCTTGCAGCG CGTCCATCTG TAGGTAAGAC
 651 TGCGTTCGCA CTTAATATTG CACAAAAGT TGCAACGCAT GAAGATATGT
 701 ATACAGTTGG TATTTTCTCG CTAGAGATGG GTGCTGATCA GTTAGCCACA
 751 CGTATGATTT GTAGTTCTGG AAATGTTGAC TCAAACCGCT TAAGAACGGG
 801 TACTATGACT GAGGAAGATT GGAGTCGTTT TACTATAGCG GTAGGTAAAT
 851 TATCACGTAC GAAGATTTTT ATTGATGATA CACCGGGTAT TCGAATTAAT
 901 GATTTACGTT CTAAATGTCG TCGATTAAAG CAAGAACATG GCTTAGACAT
 951 GATTGTGATT GACTACTTAC AGTTGATTCA AGGTAGTGGT TCACGTGCGT
 1001 CCGATAACAG ACAACAGGAA GTTTCTGAAA TCTCTCGTAC ATTAAGAGCA
 1051 TTAGCCCGTG AATTAGAATG TCCAGTTATC GCATTAAGTC AGTTATCTCG

09689952-101200

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1101 TGGTGTGAA CAACGACAAG ATAAACGTCC AATGATGAGT GATATTCGTG
1151 AATCTGGTTC GATTGAGCAA GATGCCGATA TCGTTGCATT CTTATACCGT
1201 GATGATTACT ATAACCGTGG CGGCGATGAA GATGATGACG ATGATGGTGG
1251 TTTTCGAGCCA CAAACGAATG ATGAAAACGG TGAAATTGAA ATTATCATTG
1301 CTAAGCAACG TAACGGTCCA ACAGGCACAG TTAAGTTACA TTTTATGAAA
1351 CAATATAATA AATTTACCGA TATCGATTAT GCACATGCAG ATATGATGTA
1401 A

```

dnaC nucleotide sequences alignment

Identical = 785/1413 (0.56), similar = 785/1413 (0.56)

Substitution matrix: 10 (matches), 0 (mismatches)

Gap penalty: - (50 + 3 * (gap length))

```

dnaC staph homolog   ATGGATAGAA TGTATGAGCA AAATCAAATG CCGCATAACA ATGAAGCTGA
dnaC B subtilis      ATGACAGACC TTCTGAATGA CCGGCTTCCT CCGCAAAATA TAGAAGCCGA
***                *      *      *      *      *      *      *      *

```

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dnaC staph homolog   ACAGTCTGTC TTAGGTTCAA TTATTATAGA TCCAGAATTG ATTAATACTA
dnaC B subtilis      ACAAGCCGTG TTAGGCGCTA TTTTTTACA GCCGCTGCT TTAACACTGG
***                *      *      *      *      *      *      *      *

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dnaC staph homolog   CTCAGGAAGT TTTGCTTCCT GAGTCGTTTT ATAGGGGTGC CCATCAACAT
dnaC B subtilis      CTTCAGAAGT ATTGATTCCA GATGATTCT ATAGAATGTC CCACCAAAAA
**                *      *      *      *      *      *      *      *

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dnaC staph homolog   ATTTTCCGTG CAATGATGCA CTTAAATGAA GATAATAAAG AAATTGATGT
dnaC B subtilis      ATCTATAATG CGATGCTGGT GCTCGGTGAC CGAGGTGAAC CGGTTGATCT
***                *      *      *      *      *      *      *      *

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dnaC staph homolog   TGTAACATTG ATGGATCAAT TATCGACGGA AGGTACGTG AATGAAGCGG
dnaC B subtilis      GGTGACAGTT ACATCAGAGC TTGCGAACAC AGACCTGCTG GAAGAAGTAG
**                *      *      *      *      *      *      *      *

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dnaC staph homolog   GTGGCCCCGA ATATCTTGCA GAGTTATCTA CAAATGTACC AACGACGCGA
dnaC B subtilis      GCGGTATTTC ATATTGACA GATATCGCAA ACTCGGTGCC GACAGCGGCT
*      *      *      *      *      *      *      *      *      *

```

```

dnaC staph homolog   AATGTTCACT ATTATACTGA TATCGTTTCT AAGCATGCAT TAAAACGTAG
dnaC B subtilis      AACATAGAAT ATTACGCGAA AATCGTTGAG GAAAAATCGA TTCTTCGCCG
**                *      *      *      *      *      *      *      *

```

```

dnaC staph homolog   ATTGATTCAA ACTGCAGATA GTATTGCCAA TGATGGATAT AATGATGAAC
dnaC B subtilis      ATTAATCAGA ACTGCGACAA CGATTGCTCA AGACGGGTAT ACCCGTGAGG
***                *      *      *      *      *      *      *      *

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```

dnaC staph homolog   TTGAACTAGA TGCGATTTTA AGTGATGCAG AACGTGCAAT TTTAGAGCTA
dnaC B subtilis      ATGAGGTCGA GGATTACTC AGTGAAGCGG AAAAAACGAT TATGGAAGTG
***                *      *      *      *      *      *      *      *

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```

dnaC staph homolog   TCATCTTCTC GTGAAAGCGA TGGCTTTAAA GACATTCGAG ACGTCTTAGG
dnaC B subtilis      GCACAGCGCA AAAACACGAG TGCTTTCCAA AATATTAAGG ACGTCTTTGT
**                *      *      *      *      *      *      *      *

```

```

dnaC staph homolog   ACAAGTGTAT GAAACAGCTG AAGAGCTTGA TCAAAATAGT GGTCAAACAC
dnaC B subtilis      CCAGACCTAT GATAATATCG AACAGCTTTA CAATCGAAAA GGTGATATCA
**                *      *      *      *      *      *      *      *

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dnaC staph homolog   CAGGTATACC TACAGGATAT CGAGATTTAG ACCAAATGAC AGCAGGGTTC
dnaC B subtilis      CGGGAATTCC AACAGGGTTT ACGGAGCTTG ACCGATGAC TGCGGGTTTC
*      *      *      *      *      *      *      *      *      *

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dnaC staph homolog   AACCGAAATG ATTTAATTAT CCTTGCAGCG CGTCCATCTG TAGGTAAGAC
dnaC B subtilis      CAGCGCAACG ACTTGATCAT TGTGGCTGCC CGTCCTTCAG TAGGGAAAAC
*      *      *      *      *      *      *      *      *      *

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dnaC staph homolog   TCGTTCGCGA CTTAATATTG CACAAAAAGT TGCAACGCAT GAAGATATGT
dnaC B subtilis      AGCCTTTGCC CTGAACATCG CACAAAACGT GGCGACGAAG ACCGAT---G
**                *      *      *      *      *      *      *      *

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002707 2555950

dnaC staph homolog	ATACAGTTGG	TATTTTCTCG	CTAGAGATGG	GTGCTGATCA	GTTAGCCACA
dnaC B subtilis	AGAGCGTAGC	GATTTTCAGT	CTTGAGATGG	GTGCCGAGCA	GCTCGTTATG
	* * * *	*****	** *	*****	* * * *
dnaC staph homolog	CGTATGATTT	GTAGTTCTGG	AAATGTTGAC	TCAAACCGCT	TAAGAACGGG
dnaC B subtilis	CGTATGCTCT	GTGCCGAGGG	AAATATCAAT	GCCCAGAATC	TCCGTACAGG
	*****	* *	**	*****	* * * *
dnaC staph homolog	TACTATGACT	GAGGAAGATT	GGAGTCGTTT	TACTATAGCG	GTAGGTAAAT
dnaC B subtilis	TAACTGACC	GAAGAGGATT	GGGGCAAGCT	GACGATGGCA	ATGGGAAGCC
	**	****	** * *	** *	* * *
dnaC staph homolog	TATCACGTAC	GAAGATTTTT	ATTGATGATA	CACCGGGTAT	TCGAATTAAT
dnaC B subtilis	TATCGAACAG	CGGGATTTAC	ATCGATGATA	CACCGGGTAT	TCGAGTGAGT
	****	*	*****	*****	*****
dnaC staph homolog	GATTTACGTT	CTAAATGTCG	TCGATTAAAG	CAAGAACATG	GCTTAGACAT
dnaC B subtilis	GAAATCCGTG	CCAAGTGCCG	CCGCTTGAAG	CAGGAAGCG	GGTGCGCAT
	** * *	* * *	** *	** *	* * *
dnaC staph homolog	GATTGTGATT	GACTACTTAC	AGTTGATTCA	AGGTAGTGGT	TCACGTGCGT
dnaC B subtilis	GATTTTGATC	GATTACCTGC	AATTGATTCA	GGGAAGCGGT	---CGTTCAA
	****	****	* * *	*****	****
dnaC staph homolog	CCGATAACAG	ACAACAGGAA	GTTTCTGAAA	TCTCTCGTAC	ATTAAAAGCA
dnaC B subtilis	AGGACAACCG	TCAGCAGGAA	GTATCTGAAA	TTCCCGTGA	ACTGAAGTCG
	** * *	** *	*****	* * *	* * *
dnaC staph homolog	TTAGCCCGTG	AATTAGAATG	TCCAGTTATC	GCATTAAGTC	AGTTATCTCG
dnaC B subtilis	ATTGCGAGGG	AGCTGCAAGT	CCCTGTTATC	GCGCTTCTC	AGCTTTCCAG
	* * *	* * *	** *	* * *	* * *
dnaC staph homolog	TGGTGTGAA	CAACGACAAG	ATAAACGTCC	AATGATGAGT	GATATTCGTG
dnaC B subtilis	GGGTGTTGAG	CAGCGTCAGG	ATAAACGTCC	GATGATGTCT	GATATCCGGG
	*****	* * *	*****	*****	* * *
dnaC staph homolog	AATCTGGTTC	GATTGAGCAA	GATGCCGATA	TCGTTGCATT	CTTATACCGT
dnaC B subtilis	AATCAGGAAG	TATCGAGCAG	GACGCCGATA	TTGTCGCGTT	CCTTTATCGT
	****	**	*****	*****	*****
dnaC staph homolog	GATGATTACT	ATAACCGTGG	CGGCGATGAA	GATGATGACG	ATGATGGTGG
dnaC B subtilis	GATGACTACT	ATGAC----	-----	-----	-----
	*****	****			
dnaC staph homolog	TTTCGAGCCA	CAAACGAATG	ATGAAAACGG	TGAAATTGAA	ATTATCATTG
dnaC B subtilis	-----	AAAGAAACCG	AGAATAAAAA	TATTATCGAA	ATTATTATCG
		**	* * *	* * *	*****
dnaC staph homolog	CTAAGCAACG	TAACGGTCCA	ACAGGCACAG	TTAAGTTACA	TTTTATGAAA
dnaC B subtilis	CCAAACAGCG	TAACGGCCCG	GTAGGAACCG	TGTCTCTTGC	GTTGTAATAA
	* * *	*****	* * *	*	* * *
dnaC staph homolog	CAATATAATA	AATTTACCGA	-----	--TATCGATT	ATGCACATGC
dnaC B subtilis	GAATACAACA	AATTCGTCAA	CCTGGAACCG	CGTTTTGATG	ACGCAGGCGT
	*****	* * *		* * *	*
dnaC staph homolog	AGATATGATG	TAA			
dnaC B subtilis	TCCGCCCGGC	GCA			
		*			

1	MTDLLNDRLP	PQNIEAEQAV	LGAIFLOPSA	LTASEVLIP	DDFYRMSHQK
51	IYNAMLVLGD	RGEPVDLTV	TSELANTDLL	EEVGGISYLT	DIANSVPTAA
101	NIEYYAKIVE	EKSILRRLIR	TATTIAQDGY	TREDEVEDLL	SEAEKTIMEV
151	AQRKNTSAFQ	NIKDVLVQTY	DNIEQLYNRK	GDITGIPTGF	TELD RMTAGF
201	QRNDLIIVAA	RPSVGKTAFA	LNIAQNVATK	TDESVAFISL	EMGAEQLVMR
251	MLCAEGNINA	QNLRTGNLTE	EDWGKLTMM	GSLSNSGIYI	DDTPGIRVSE
301	IRAKCRRLKQ	ESGLGMILID	YLQLIQSGSR	SKDNRQQEVS	EISRELKSIA
351	RELQVPVIAL	SQLSRGVEQR	QDKRPMMSDI	RESGSIEQDA	DIVAFLYRDD
401	YYDKETENKN	IIEIIIAKQR	NGPVGTVSLA	FVKEYNKFVN	LERRFDDAGV
451	PPGA				

1	MDRMYEQNQM	PHNNEAEQSV	LGSIIIDPEL	INTTQEVLLP	ESFYRGAHQH
51	IFRAMMHLNE	DNKEIDVVTL	MDQLSTEGTL	NEAGGPQYLA	ELSTNVPTTR
101	NVQYYTDIVS	KHALKRRLIQ	TADSIANDGY	NDELELDAIL	SDAERRILEL
151	SSSRESDGFK	DIRDVLGQVY	ETAEELDQNS	GQTPGIPTGY	RDLDQMTAGF
201	NRNDLIILAA	RPSVGKTAF	LNIAQKVATH	EDMYTVGIFS	LEMGADQLAT
251	RMICSSGNVD	SNRLRTGTMT	EEDWSRFTIA	VGKLSRTKIF	IDDTPGIRIN
301	DLRSKCRRLK	QEHGLDMIVI	DYLQLIQSGS	SRASDNRQQE	VSEISRTLKA
351	LARELECPVI	ALSQLSRGVE	QRQDKRPMMS	DIRESGSIEQ	DADIVAFLYR
401	DDYYNRGGDE	DDDDGGFEP	QTNDENGEIE	IIIAKQRNGP	TGTVKLHFMK
451	QYNKFTDIDY	AHADMM			

Identical = 265/471 (0.56), similar = 345/471 (0.73)
Substitution matrix: blosum62
Gap penalty: - (11 + 1 * (gap length))

dnaC Staph homolog	MDRMYEQNM	PHNNEAEQSV	LGSIIIDPEL	INTTQEVLLP	ESFYRGAHQH
dnaC B subtilis	MTDLLNDRLP	PQNIEAEQAV	LGAIFLQPSA	LTLLASEVLIP	DDFYRMSHQK
	* +	* * * * * +	**+* + *	+ * * * +	+ * * * + **
dnaC Staph homolog	IFRAMMHLNE	DNKEIDVVTL	MDQLSTEGTL	NEAGGPQYLA	ELSTNVPTTR
dnaC B subtilis	IYNAMLVLGD	RGEVDLVTV	TSELANTDLL	EEVGGISYLT	DIANSVPTAA
	*+ *+* * +	+ + * * * +	+*+ *	* * * * *	+++ + * * *
dnaC Staph homolog	NVQYYTDIVS	KHALKRRLIQ	TADSIANDGY	NDELELDAIL	SDAERRILEL
dnaC B subtilis	NIEYYAKIVE	EKSILRRLIR	TATTIAQDGY	TREDEVEDLL	SEAEKTIMEV
	++* * *	+ + * * * +	** + * * * *	* *+* + *	*+*+* +*+*
dnaC Staph homolog	SSSRESDGFK	DIRDVLGQVY	ETAEELDQNS	GQTPGIPTGY	RDLDMQMTAGF
dnaC B subtilis	AQRKNTSAFQ	NIKDVLVQTY	DNIEQLYNRK	GDITGIPTGF	TELDRLMTAGF
	+ + + *+	+*+* * * *	+ *+*	* * * * * +	+*+*+* * *
dnaC Staph homolog	NRNDLIILAA	RPSVGKTAF	LNIAQKVATH	EDMYTVGIFS	LEMGAQDLAT
dnaC B subtilis	QRNDLIIVAA	RPSVGKTAF	LNIAQNVATH	TD-ESVAIFS	LEMGAELQVM
	* * * * * + *	* * * * * * * *	* * * * * * *	* + * * *	* * * * * + * *
dnaC Staph homolog	RMICSSGNVD	SNRLRTGTMT	EEDWSRFTIA	VGKLSRTKIF	IDDTPGIRIN
dnaC B subtilis	RMLCAEGNIN	AQNLRGTGNT	EEDWGKLTMA	MGSLNSNGIY	IDDTPGIRVS
	++* +*+*	+ * * * +	* * * * + *+*	+* * * + *	* * * * * + *

dnaC Staph homolog
dnaC B subtilis

DLRSKCRLK QEHGLDMIVI DYQLIQSG SRASDNRQE VSEISRTLKA
EIRAKCRLK QESGLGMILI DYQLIQSG -RSKDNRQE VSEISRELKS
++++***** ** ** ** *+ ***** **+ ***** **+

dnaC Staph homolog
dnaC B subtilis

LARELECPVI ALSQLSRGVE QRQDKRPMMS DIRESGSIEQ DADIVAFLYR
IARELQVPVI ALSQLSRGVE QRQDKRPMMS DIRESGSIEQ DADIVAFLYR
+*****+ *** ***** ***** ***** *****

dnaC Staph homolog
dnaC B subtilis

DDYYNRGGDE DDDDDGGFEP QTNDENGEIE IIIAKQRNGP TGTVKLHFMK
DDYYDK---- ----- ETENKN-IIIE IIIAKQRNGP VGTVSLAFVK
*****+ **++* ** ***** ** * **+

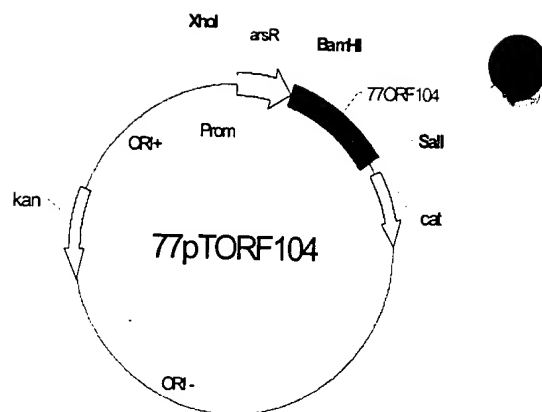
dnaC Staph homolog
dnaC B subtilis

QYNKFTDIDY AHADM----- M
EYNKFVNLER RFDDAGVPPG A
*****++ *

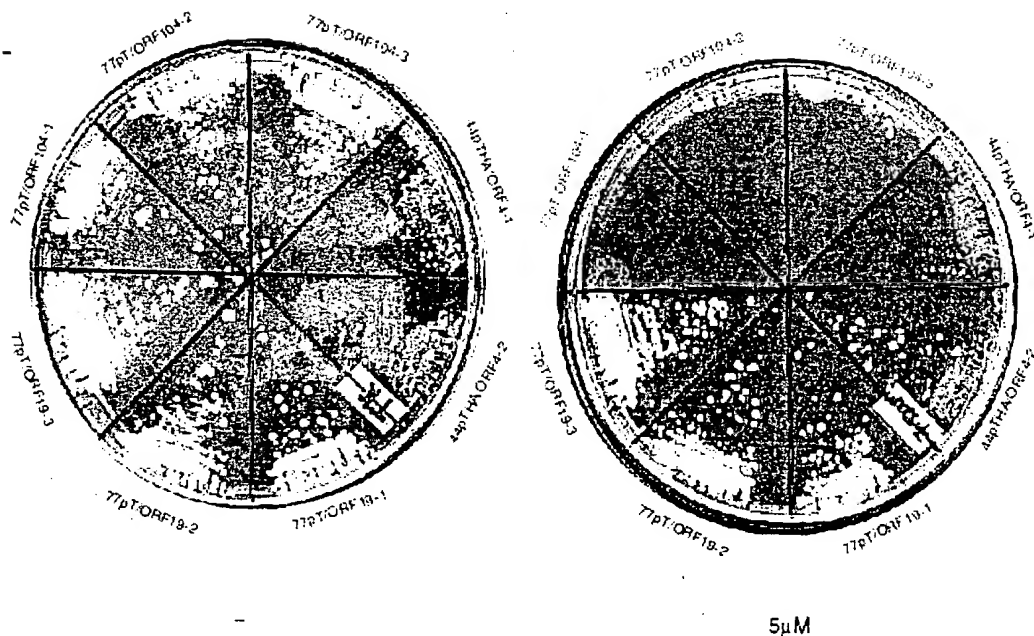
002707 2568960

FIGURE 7

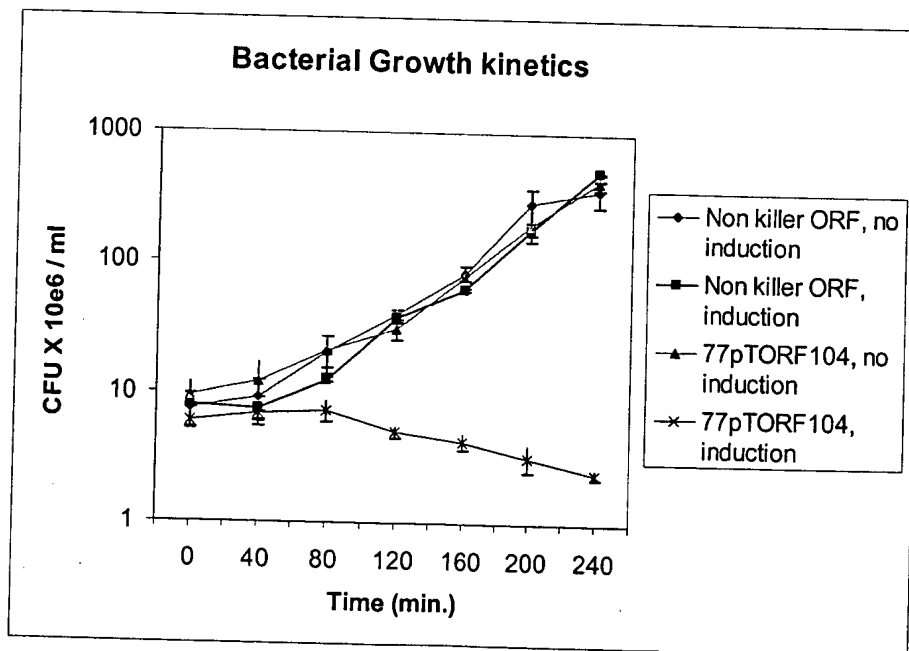
A-



B-



C-

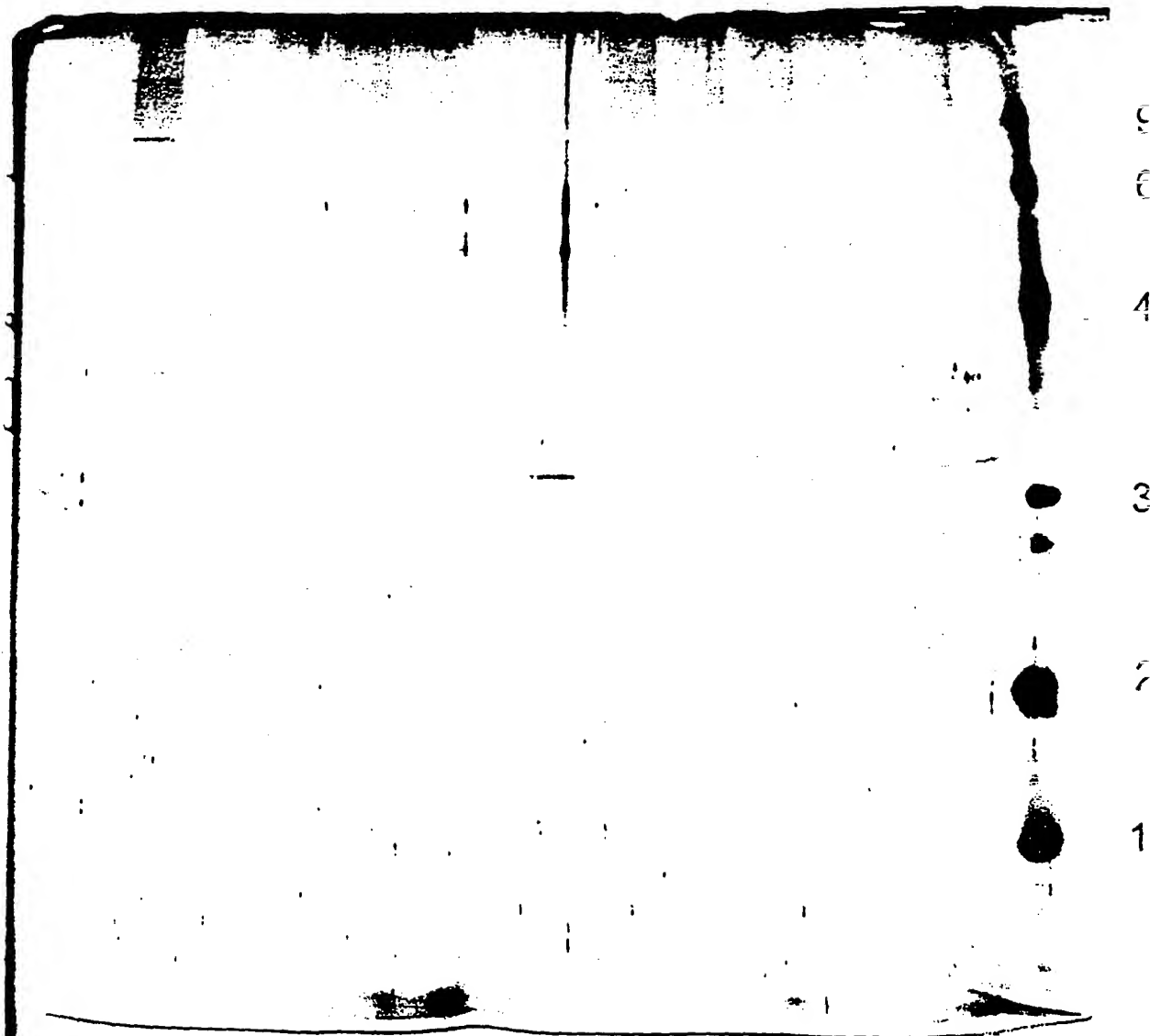


GST

GST/ ORF104

ACB 0 0.1 0.5 1.0 2.0

ACB 0 0.1 0.5 1.0 2.0 Mr



002101"25668960

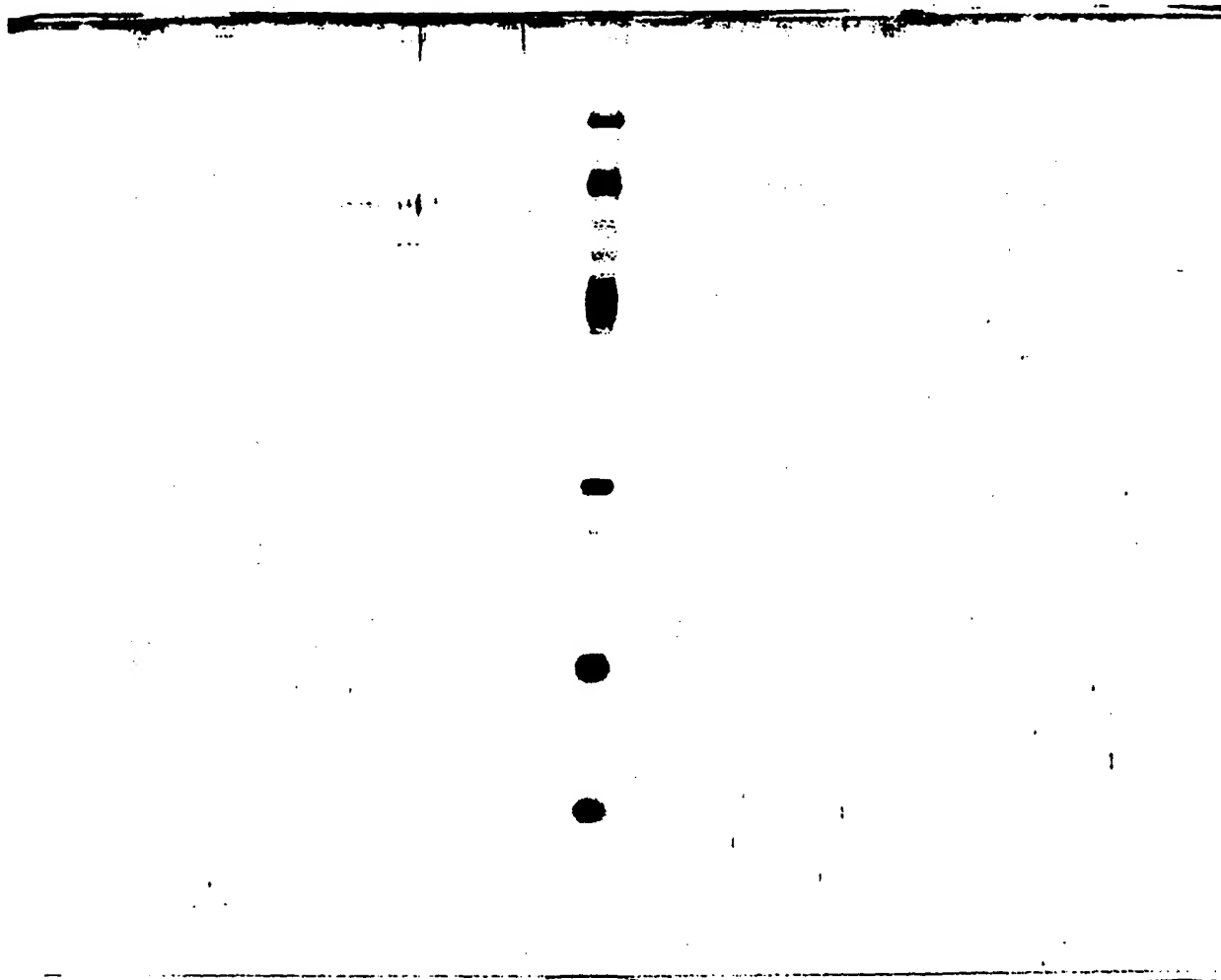
Fig. 8 A

GST

GST/ ORF104

ACB 0 0.1 0.5 1.0 2.0 Mr

ACB 0 0.1 0.5 1.0 2.0



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8B

GST

GST/ ORF104

Mr ACB 0 0.1 0.5 1.0 2.0 ACB 0 0.1 0.5 1.0 2.0

97

66

45

30

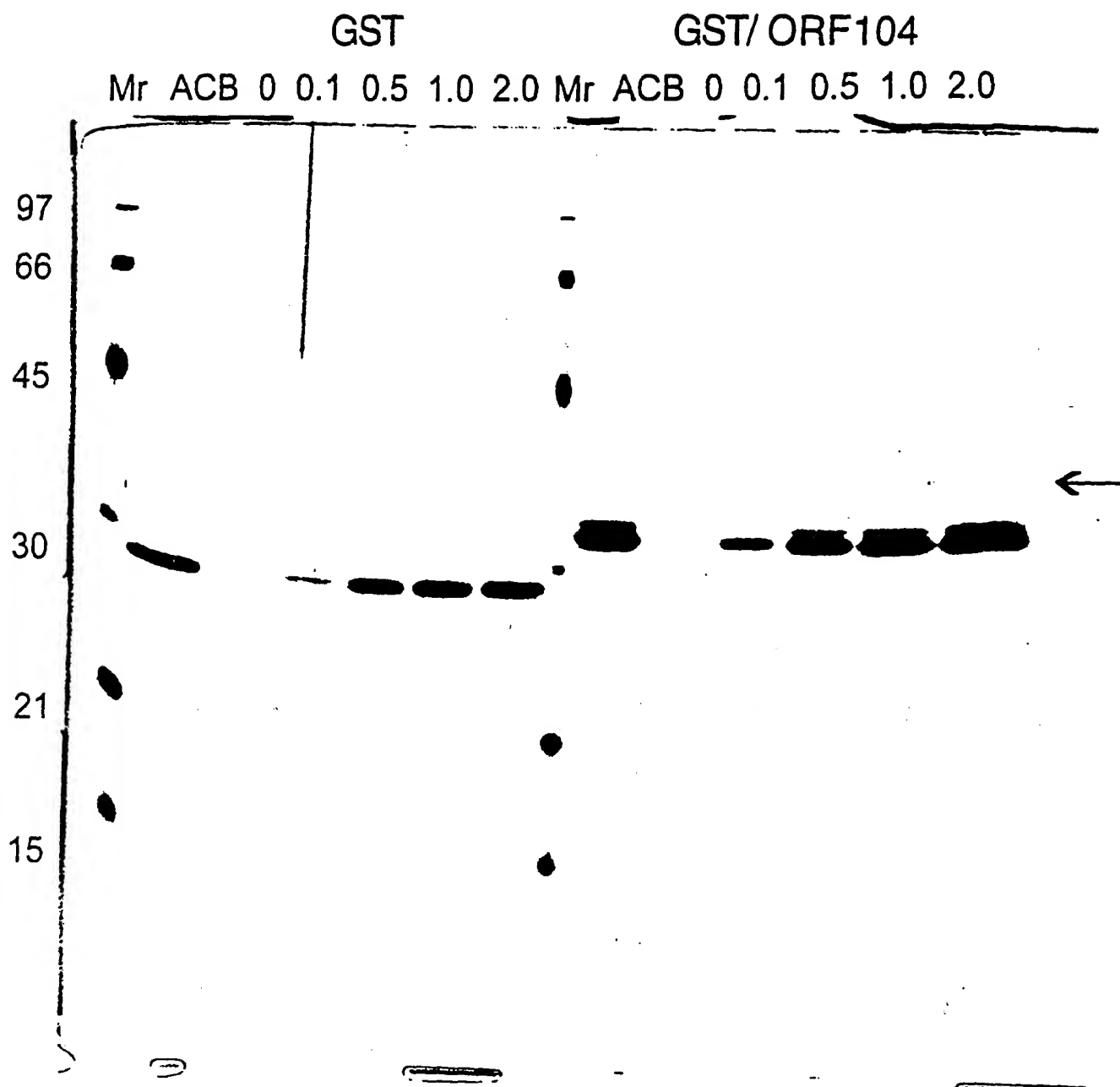
21

15

002101-25668960

8C

002101" 25668960



002707 2565950

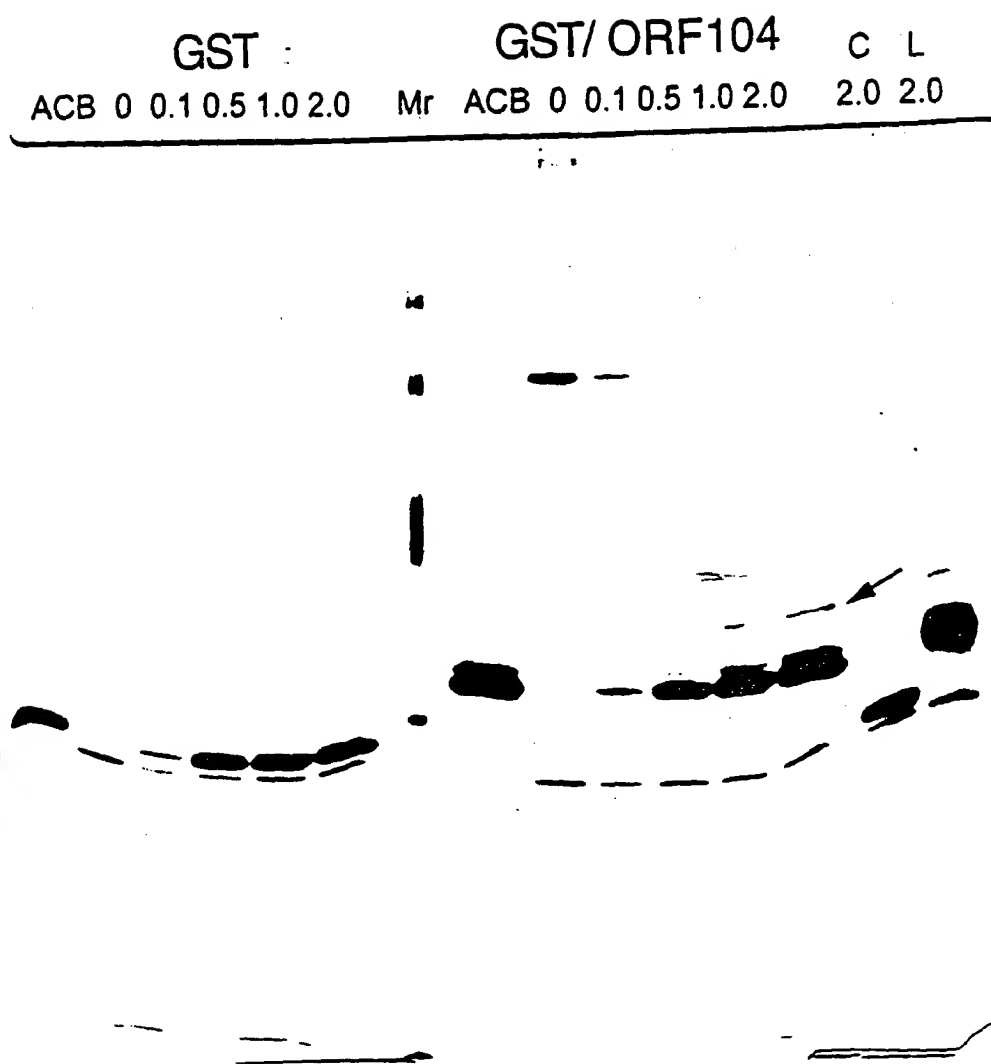


Fig. 9

002TOT*25658960

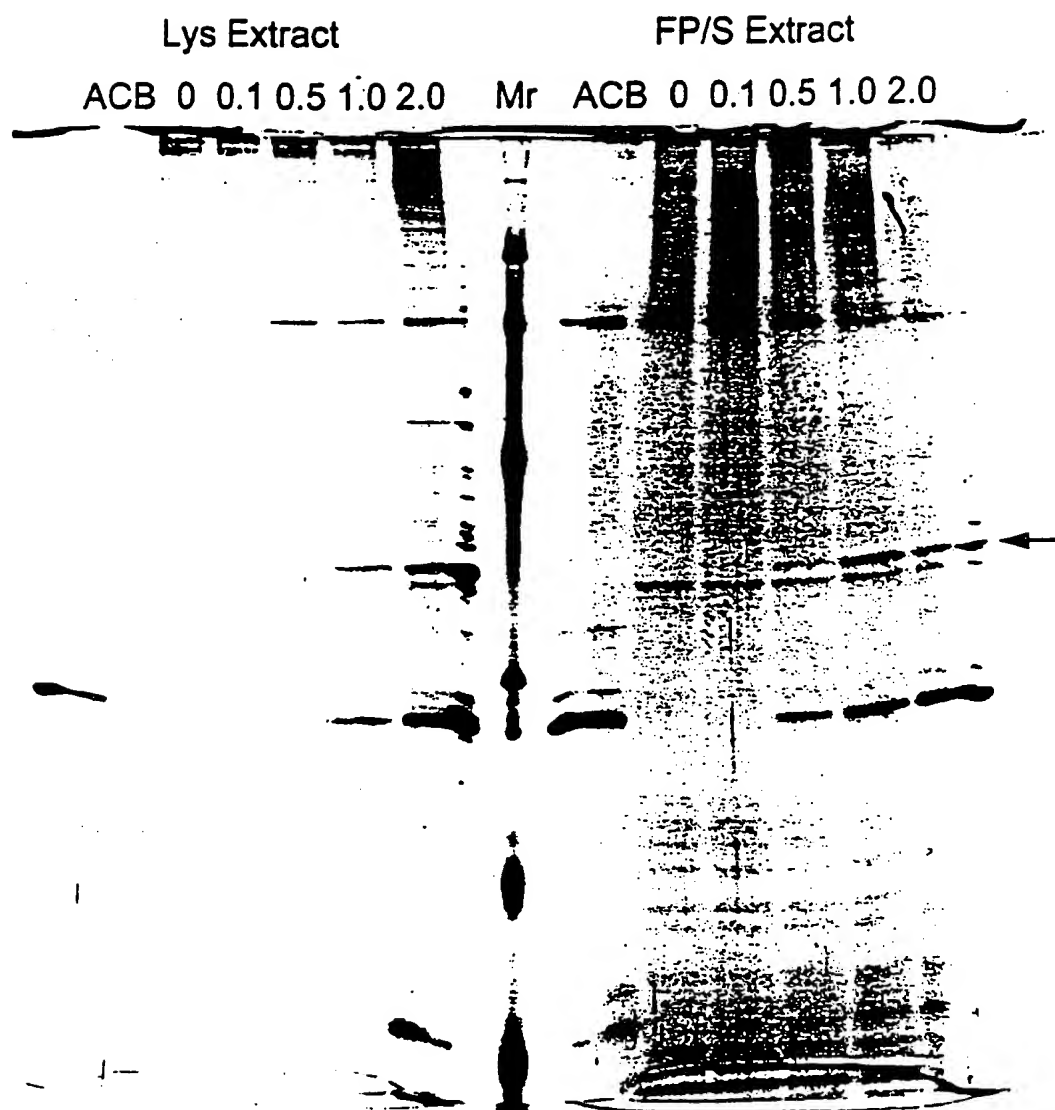
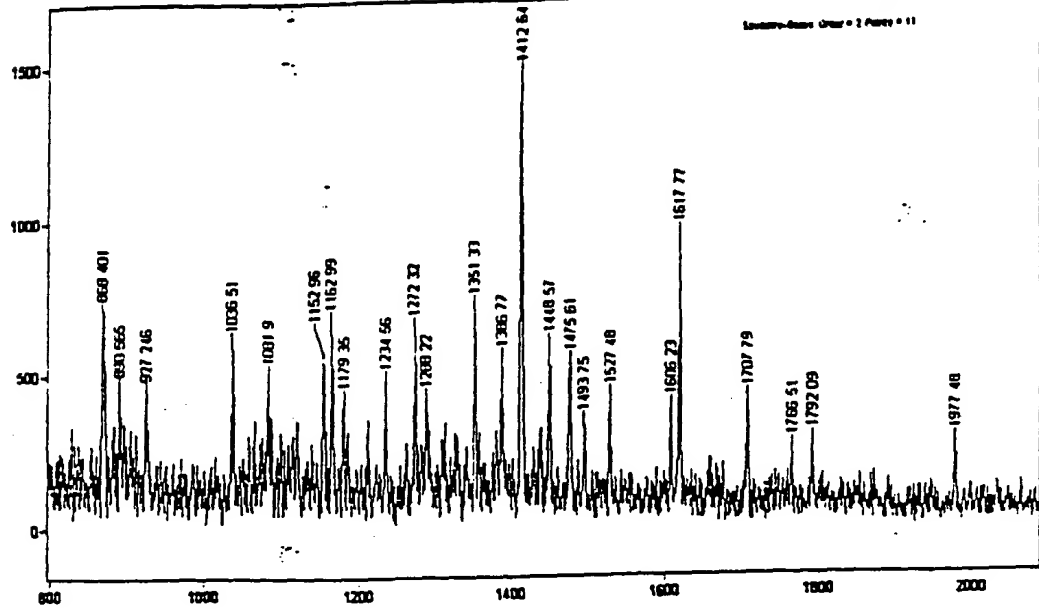


Fig. 10

Original Filename: C:\BIOREAL\DATA\PHAGE7-1\SMOOTH.MS
This File # 1: C:\BIOREAL\DATA\PHAGE7-1\SMOOTH.MS
Comment: Page 1 from 51

Method: L251252A
Scan: 1000
Acquiring Voltage: 2000V
Out Voltage: 04.800 V
Duty Cycle Voltage: 0.070 V
Duty: 170.0 Hz
Spectrum: 14
Laser: 1070
Scan Average: 14
Pressure: 3.21e-4
Low Mass Gate: OFF
Tuned on Acceptor: 20.0 OFF
Negative Ion: OFF
Collision: 60.00 V.12 MS



ii) Tryptic peptide mass spectrum of interacting protein (1% SDS eluate)

Original Filename: C:\BIOREAL\DATA\PHAGE7-1\SMOOTH.MS
This File # 1: C:\BIOREAL\DATA\PHAGE7-1\SMOOTH.MS
Comment: Page 525 1

Method: L251252A
Scan: 1000
Acquiring Voltage: 2000V
Out Voltage: 04.800 V
Duty Cycle Voltage: 0.070 V
Duty: 170.0 Hz
Spectrum: 14
Laser: 1070
Scan Average: 142
Pressure: 3.21e-4
Low Mass Gate: OFF
Tuned on Acceptor: 20.0 OFF
Negative Ion: OFF
Collision: 60.00 V.12 MS

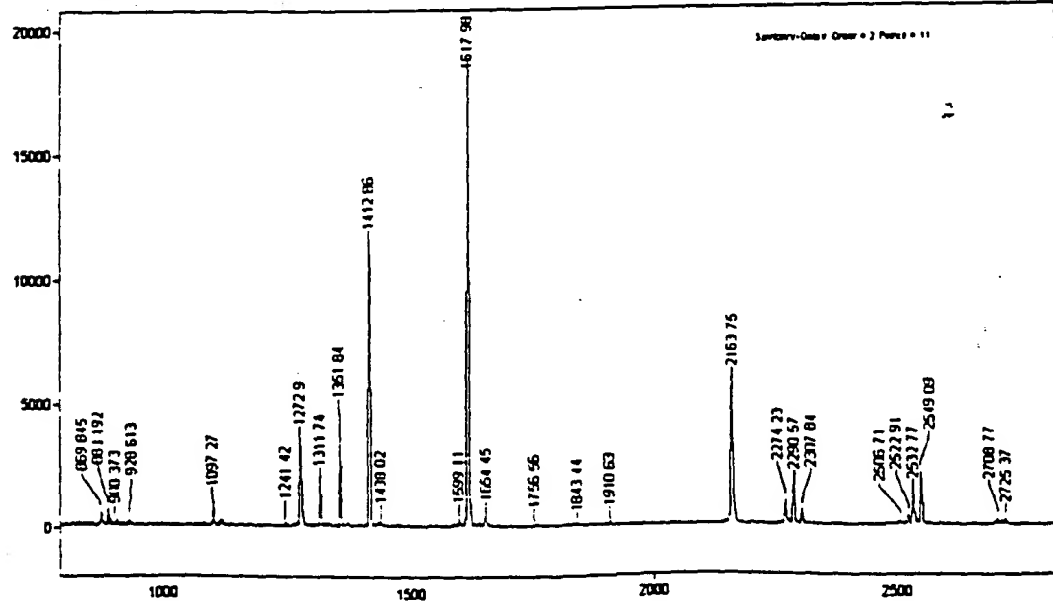
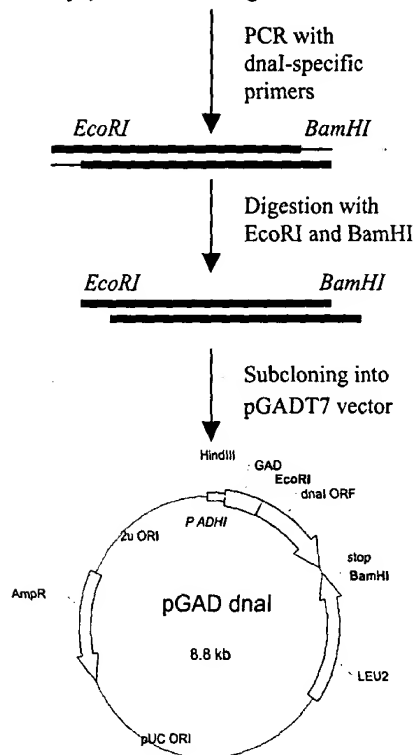
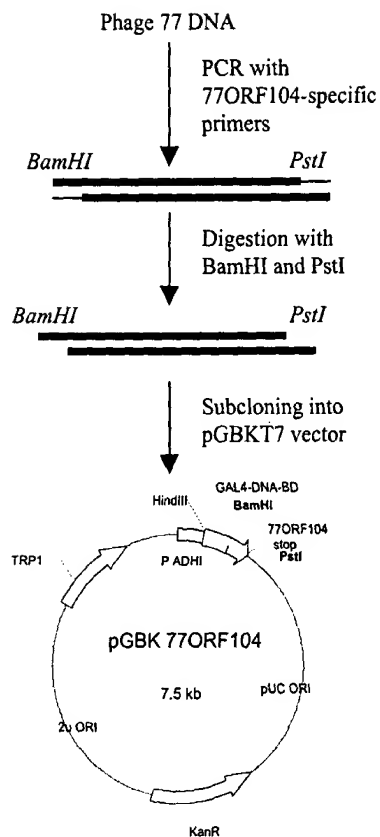


Fig. 11

A- *Staphylococcus aureus* genomic DNA



B-



C-

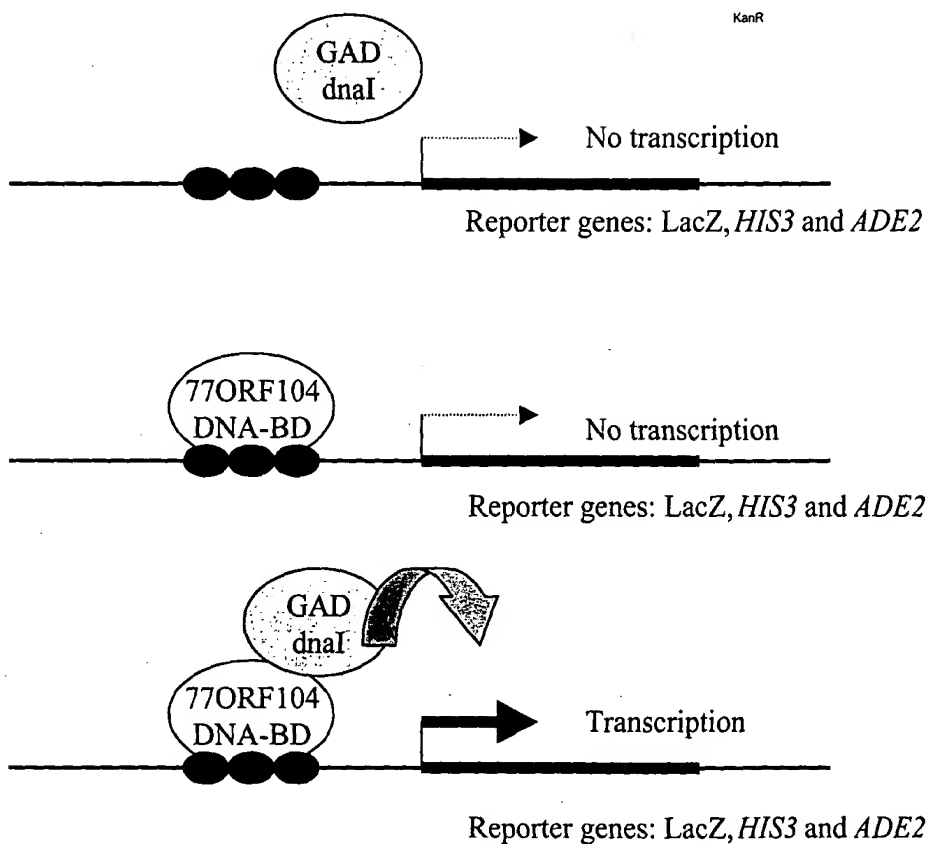
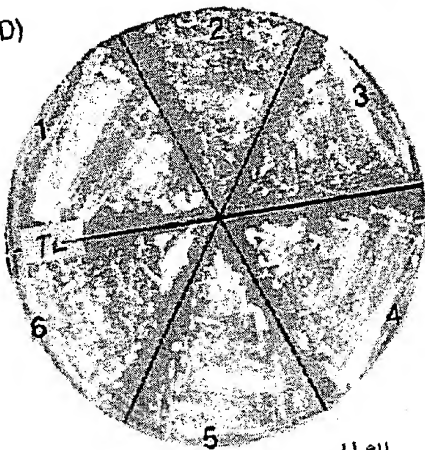
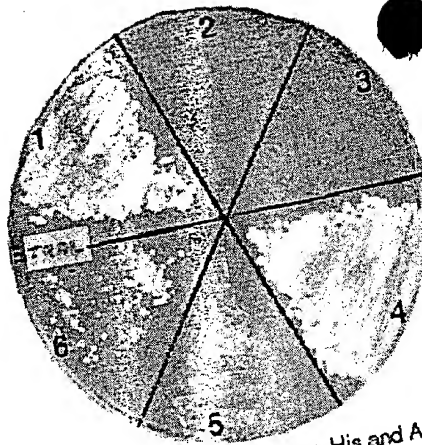


Fig. 12 D + E

D)



SD plate without Trp and Leu

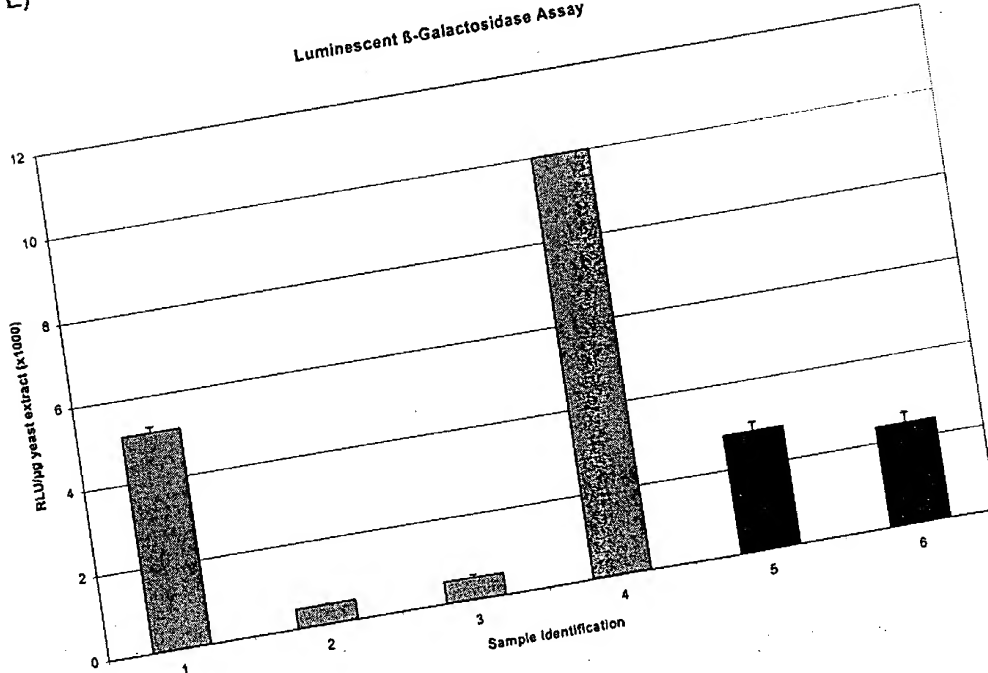


SD plate without Trp, Leu, His and Ade

- 1) pGBKT7-53 and pGADT7-T
- 2) pGBKT7-53 and pGAD dna I
- 3) pGBKT7ORF104 and pGADT7-T
- 4) pGBKT7-LAM and pCL1
- 5) pGBKT7ORF104 and pGAD dna I
- 6) pGBK dna I and pGAD77ORF104

E)

Luminescent β -Galactosidase Assay



002101 22668950

Effect of 77ORF 104 expression on ³H-Thymidine incorporation

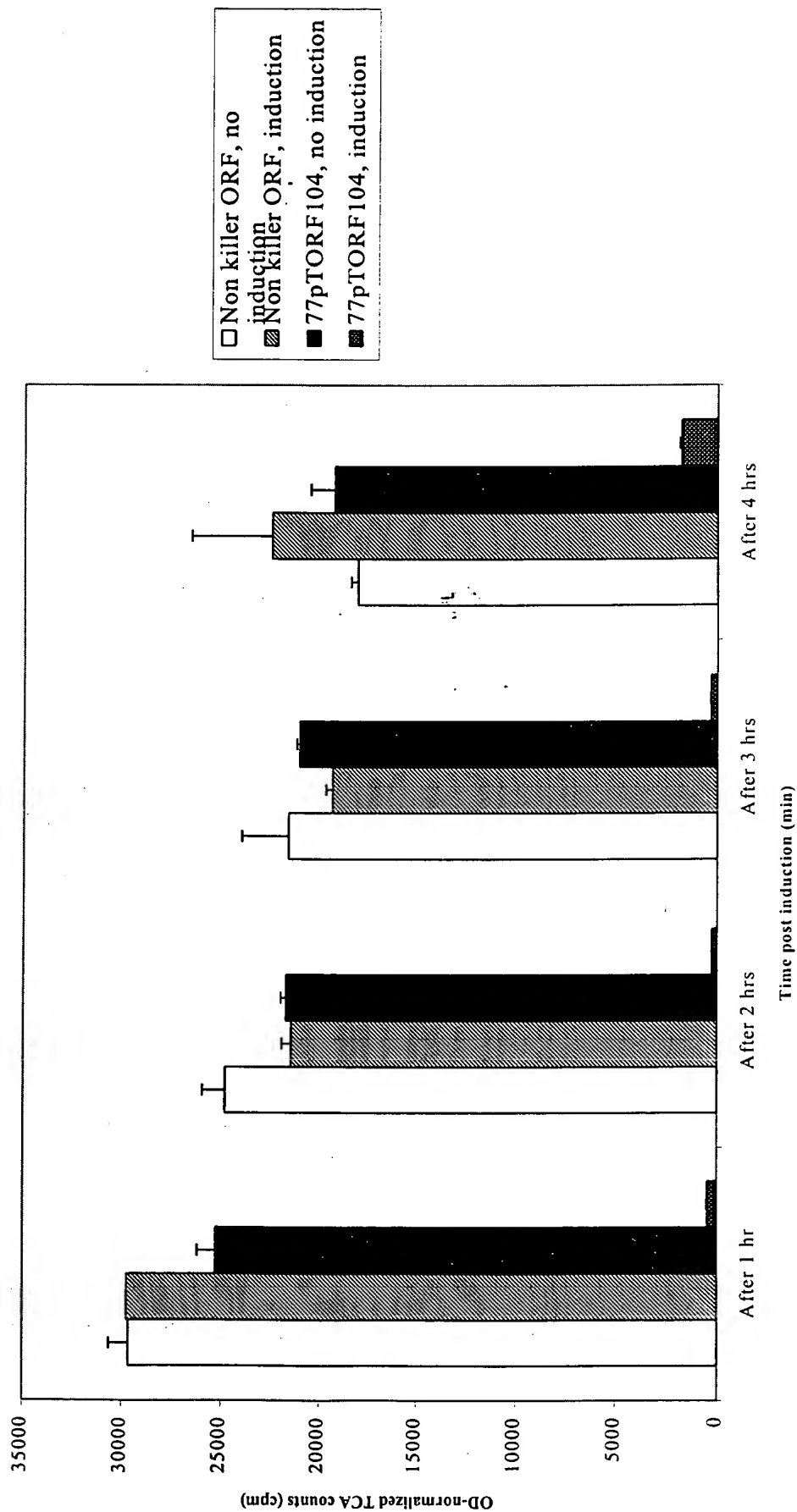
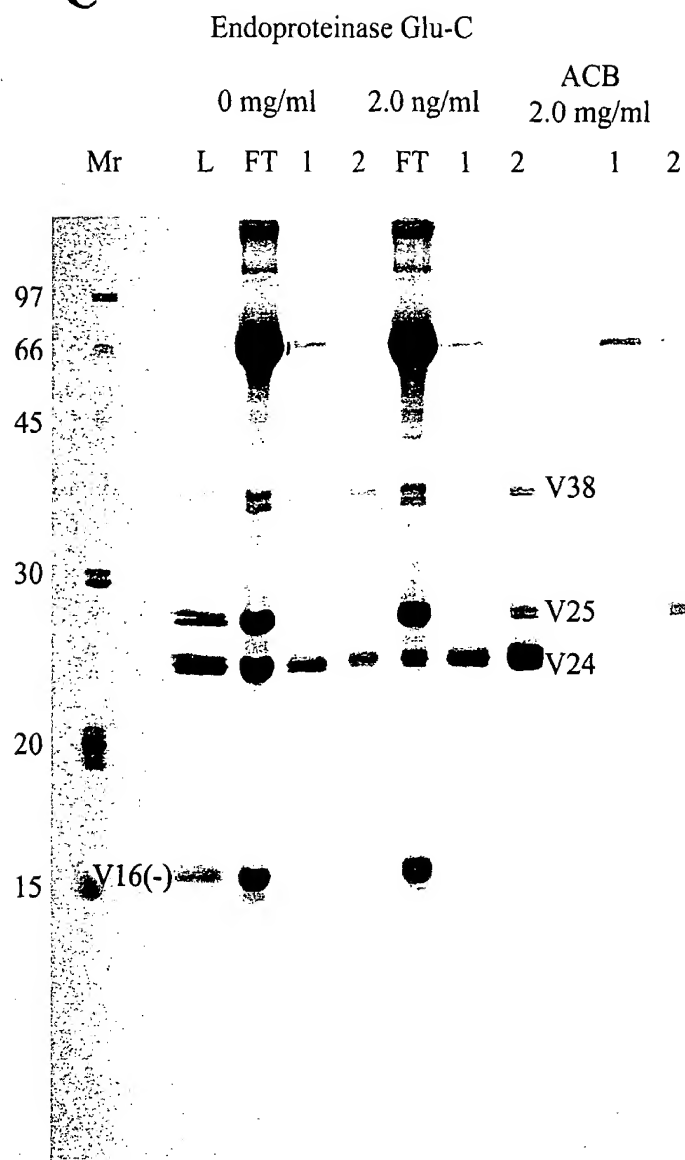


FIGURE 14A

C



002TOT 25658260

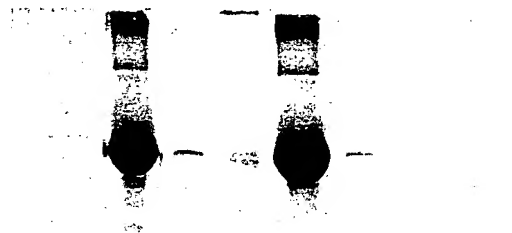
URE 14B

Chymotrypsin

0 mg/ml

2.0 ng/ml

L FT 1 2 FT 1 2



C38

C25
C24
C23
C22
C21
C20

C16(-)
C15(-)

C14

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FIGURE 14C

Amino acid residues corresponding to interacting partial proteolytic fragments.

Protease	Proteolytic fragment ID (from Fig. 14A, B)	ID of SEQ ID NO: 2 fragment interacting with 77ORF104	
		from amino	to carboxyl
Endoproteinase Glu-C	V24	117	313
	V24	119	313
Chymotrypsin	C38	12	313
	C25	83	313
	C24	77	305
	C23	77	304
	C22	116	313
	C21	131	313
SEQ ID NO: 2	Complete	1	313

002101" 25658960

FIGURE 15

SEQ ID NO: 16

>S.aureus dnaI : amino acid 150-313

AADDICTAITNGEQVKGLYLYGPFGTGKSFILGAIANQLKSKKVRSTIIYLPFIRTLKG
GFKDGSFEKKLHRVREANILMLDDIGAEVTPWVRDEVIGPLLHYRMVHELPTFFSSNFD
YSELEHHLAMTRDGEEKTKAARIIERVKSLSTPYFLSGENFRNN

SEQ ID NO: 17

>S.aureus dnaI : nucleotide 448-942

gcagcagatgatattgtacagcaataactaatggggaacaagtgaaggcctttacctt
tatgggtccatttgggacaggtaaatcttttattctaggtgcaattgcgaatcagctcaaa
tctaagaagggtacgttcgacaattatttattaccggaatttattagaacattaaaaggt
ggctttaagatggttcttttgaagaattacatcgcgtaagagaagcaaacatttta
atgcttgatgatattggggctgaagaagtgactccatgggtgagagatgaggttaattgga
cctttgctacattatcgatgggtcatgaattaccaacattcttagttctaattttgac
tatagtgaattggaacatcatttagcgatgactcgtgatggtgaagagaagactaaagca
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ttcagaacaattga

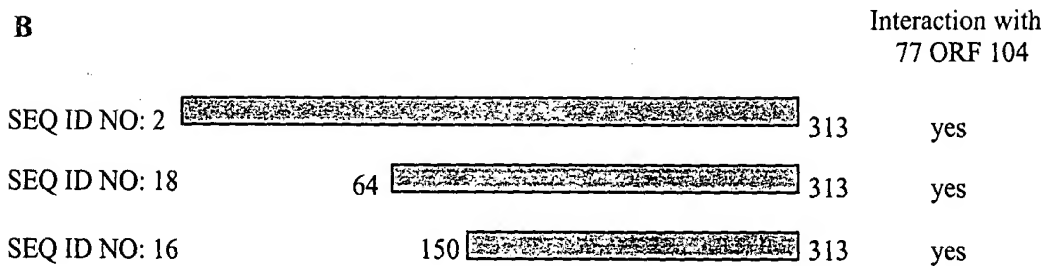
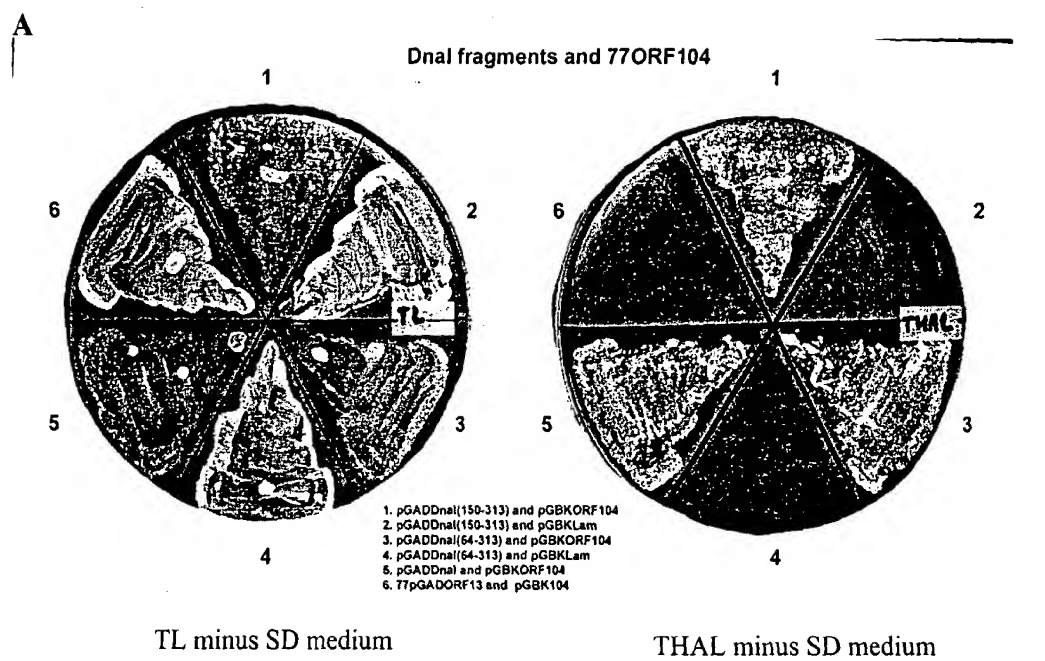
SEQ ID NO: 18

>S.aureus dnaI : amino acid 64-313

YKDQQKHYDGHKFADCPNFVKGHVPELYVDNNRIKIRYLQCPCKIKYDEERFEAELITSHH
MQRDTLNAKLKDIYMNHRDLVDVMAADDICTAITNGEQVKGLYLYGPFGTGKSFILGAI
ANQLKSKKVRSTIIYLPFIRTLKGGFKDGSFEKKLHRVREANILMLDDIGAEVTPWVR
DEVIGPLLHYRMVHELPTFFSSNFDYSELEHHLAMTRDGEEKTKAARIIERVKSLSTPYF
LSGENFRNN

09689952-101200

FIGURE 16



09669667.101200